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RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/09/966,561

TIME: 10:29:11

Input Set : N:\Crf3\RULE60\09966561.raw

Output Set: N:\CRF3\01142002\I966561.raw

1 <110> APPLICANT: University of Southern California
 2 Miller, Carol A.
 3 Dong, Zhao Hui
 4 Zhang, Yan
 5 <120> TITLE OF INVENTION: APOPTOSIS INHIBITION
 6 <130> FILE REFERENCE: 13761-724
 7 <140> CURRENT APPLICATION NUMBER: US/09/966,561
 8 <141> CURRENT FILING DATE: 2001-09-27
 9 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/419,694
 W--> 10 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-10-14
 11 <160> NUMBER OF SEQ ID NOS: 3
 12 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 2836
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Homo sapiens
 18 <220> FEATURE:
 19 <221> NAME/KEY: CDS
 20 <222> LOCATION: (1)...(2136)
 21 <400> SEQUENCE: 1

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23	Met Ala Glu Arg Glu Ser Gly Gly Leu Gly Gly Gly Ala Ala Ser Pro	
24	1 5 10 15	
25	ccc gcc gcc tcc ccg ttc ctg ggg ctg cac atc gct tcg cct ccc aat	96
26	Pro Ala Ala Ser Pro Phe Leu Gly Leu His Ile Ala Ser Pro Pro Asn	
27	20 25 30	
28	ttc agg ctc acc cat gac atc agc ctg gag gag ttt gag gat gaa gac	144
29	Phe Arg Leu Thr His Asp Ile Ser Leu Glu Glu Phe Glu Asp Glu Asp	
30	35 40 45	
31	ctc tcg gag atc act gat gag tgt ggc atc agc tta cag tgc aaa gac	192
32	Leu Ser Glu Ile Thr Asp Glu Cys Gly Ile Ser Leu Gln Cys Lys Asp	
33	50 55 60	
34	acc ctg tcc tta cgg ccc ccg cgc gcc ggg ctg ctc tct gcg ggc ggc	240
35	Thr Leu Ser Leu Arg Pro Pro Arg Ala Gly Leu Leu Ser Ala Gly Gly	
36	65 70 75 80	
37	ggc ggc gcg ggg agc cgg ttg cag gcc gag atg ctg cag atg gac ctg	288
38	Gly Gly Ala Gly Ser Arg Leu Gln Ala Glu Met Leu Gln Met Asp Leu	
39	85 90 95	
40	atc gac gcg acg ggg gac act ccc ggg gcc gag gac gac gag gag gac	336
41	Ile Asp Ala Thr Gly Asp Thr Pro Gly Ala Glu Asp Asp Glu Glu Asp	
42	100 105 110	
43	gac gac gag gag cgc gcg gcc cgg cgg ccg gga gcg ggg ccg ccc aag	384
44	Asp Asp Glu Glu Arg Ala Ala Arg Arg Pro Gly Ala Gly Pro Pro Lys	
45	115 120 125	
46	gcc gaa tcc ggc cag gag ccg gcg tcc cgc ggc cag ggc cag agc caa	432
47	Ala Glu Ser Gly Gln Glu Pro Ala Ser Arg Gly Gln Gly Gln Ser Gln	
48	130 135 140	

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49	ggc cag agc cag ggc ccg ggc agc ggg gac acg tac cgg ccc aag cgg	480
50	Gly Gln Ser Gln Gly Pro Gly Ser Gly Asp Thr Tyr Arg Pro Lys Arg	
51	145 150 155 160	
52	ccc acc acg ctc aac ctc ttt ccg cag gtg ccg cgg tct cag gac aca	528
53	Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln Asp Thr	
54	165 170 175	
55	ctg aat aat aat tct ctg ggc aaa aag cac agt tgg cag gat cgg gtg	576
56	Leu Asn Asn Asn Ser Leu Gly Lys Lys His Ser Trp Gln Asp Arg Val	
57	180 185 190	
58	tct cga tca tcc tca ccc ctg aag aca ggg gag cag aca cca ccg cat	624
59	Ser Arg Ser Ser Ser Pro Leu Lys Thr Gly Glu Gln Thr Pro Pro His	
60	195 200 205	
61	gaa cac atc tgc ctg agc gag gag ctg ccc ccc cag agc ggc ccc gcc	672
62	Glu His Ile Cys Leu Ser Glu Glu Leu Pro Pro Gln Ser Gly Pro Ala	
63	210 215 220	
64	ccc acc aca gat cga ggc acc tcc acc gac agc cct tgc cgc cgc agc	720
65	Pro Thr Thr Asp Arg Gly Thr Ser Thr Asp Ser Pro Cys Arg Arg Ser	
66	225 230 235 240	
67	aca gcc acc cag atg gca cct ccg ggt ggt ccc cct gct gcc ccg cct	768
68	Thr Ala Thr Gln Met Ala Pro Pro Gly Gly Pro Pro Ala Ala Pro Pro	
69	245 250 255	
70	ggg ggt cgg ggc cac tcg cat cga gac cga atc cac tac cag gcc gat	816
71	Gly Gly Arg Gly His Ser His Arg Asp Arg Ile His Tyr Gln Ala Asp	
72	260 265 270	
73	gtg cga cta gag gcc act gag gag atc tac ctg acc cca gtg cag agg	864
74	Val Arg Leu Glu Ala Thr Glu Glu Ile Tyr Leu Thr Pro Val Gln Arg	
75	275 280 285	
76	ccc cca gac gct gca gag ccc acc tcc gcc ttc ctg ccg ccc act gag	912
77	Pro Pro Asp Ala Ala Glu Pro Thr Ser Ala Phe Leu Pro Pro Thr Glu	
78	290 295 300	
79	agc cgg atg tca gtc agc tcc gat cca gac cct gcc gcc tac ccc tcc	960
80	Ser Arg Met Ser Val Ser Ser Asp Pro Asp Pro Ala Ala Tyr Pro Ser	
81	305 310 315 320	
82	acg gca ggg cgg ccg cac ccc tcc atc agt gaa gag gaa gag ggc ttc	1008
83	Thr Ala Gly Arg Pro His Pro Ser Ile Ser Glu Glu Glu Glu Gly Phe	
84	325 330 335	
85	gac tgc ctg tcg tcc ccagag cgg gct gag ccc cca ggc gga ggg tgg	1056
86	Asp Cys Leu Ser Ser Pro Glu Arg Ala Glu Pro Pro Gly Gly Gly Trp	
87	340 345 350	
88	cgg ggg agc ctg ggg gag ccg ccg cca cct cca cgg gcc tct ctg agc	1104
89	Arg Gly Ser Leu Gly Glu Pro Pro Pro Pro Pro Arg Ala Ser Leu Ser	
90	355 360 365	
91	tcg gac acc agc gcc ctg tcc tat gac tct gtc aag tac acg ctg gtg	1152
92	Ser Asp Thr Ser Ala Leu Ser Tyr Asp Ser Val Lys Tyr Thr Leu Val	
93	370 375 380	
94	gta gat gag cat gca cag ctg gag ctg gtg agc ctg cgg ccg tgc ttc	1200
95	Val Asp Glu His Ala Gln Leu Glu Leu Val Ser Leu Arg Pro Cys Phe	
96	385 390 395 400	
97	gga gac tac agt gac gag agt gac tct gcc acc gtc tat gac aac tgt	1248

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Input Set : N:\Cr3\RULE60\09966561.raw

Output Set: N:\CRF3\01142002\I966561.raw

98	Gly Asp Tyr Ser Asp Glu Ser Asp Ser Ala Thr Val Tyr Asp Asn Cys	
99	405 410 415	
100	gcc tcc gtc tcc tcg ccc tat gag tcg gcc atc gga gag gaa tat gag	1296
101	Ala Ser Val Ser Ser Pro Tyr Glu Ser Ala Ile Gly Glu Glu Tyr Glu	
102	420 425 430	
103	gag gcc ccg cgg ccc cag ccc cct gcc tgc ctc tcc gag gac tcc acg	1344
104	Glu Ala Pro Arg Pro Gln Pro Pro Ala Cys Leu Ser Glu Asp Ser Thr	
105	435 440 445	
106	cct gat gaa ccc gac gtc cat ttc tcc aag aaa ttc ctg aac gtc ttc	1392
107	Pro Asp Glu Pro Asp Val His Phe Ser Lys Lys Phe Leu Asn Val Phe	
108	450 455 460	
109	atg agt ggc cgc tcc cgc tcc tcc agt gct gag tcc ttc ggg ctg ttc	1440
110	Met Ser Gly Arg Ser Arg Ser Ser Ser Ala Glu Ser Phe Gly Leu Phe	
111	465 470 475 480	
112	tcc tgc atc atc aac ggg gag gag cag gag cag acc cac cgg gcc ata	1488
113	Ser Cys Ile Ile Asn Gly Glu Glu Gln Glu Gln Thr His Arg Ala Ile	
114	485 490 495	
115	ttc agg ttt gtg cct cga cac gaa gac gaa ctt gag ctg gaa gtg gat	1536
116	Phe Arg Phe Val Pro Arg His Glu Asp Glu Leu Glu Leu Glu Val Asp	
117	500 505 510	
118	gac cct ctg cta gtg gag ctc cag gct gaa gac tac tgg tac gag gcc	1584
119	Asp Pro Leu Leu Val Glu Leu Gln Ala Glu Asp Tyr Trp Tyr Glu Ala	
120	515 520 525	
121	tac aac atg cgc act ggt gcc cgg ggt gtc ttt cct gcc tat tac gcc	1632
122	Tyr Asn Met Arg Thr Gly Ala Arg Gly Val Phe Pro Ala Tyr Tyr Ala	
123	530 535 540	
124	atc gag gtc acc aag gag ccc gag cac atg gca gcc ctg gcc aaa aac	1680
125	Ile Glu Val Thr Lys Glu Pro Glu His Met Ala Ala Leu Ala Lys Asn	
126	545 550 555 560	
127	agt gac tgg gtg gac cag ttc cgg gtg aag ttc ctg ggc tca gtc cag	1728
128	Ser Asp Trp Val Asp Gln Phe Arg Val Lys Phe Leu Gly Ser Val Gln	
129	565 570 575	
130	gtt ccc tat cac aag ggc aat gac gtc ctc tgt gct gct atg caa aag	1776
131	Val Pro Tyr His Lys Gly Asn Asp Val Leu Cys Ala Ala Met Gln Lys	
132	580 585 590	
133	att gcc acc acc cgc cgg ctc acc gtg cac ttt aac ccg ccc tcc agc	1824
134	Ile Ala Thr Thr Arg Arg Leu Thr Val His Phe Asn Pro Pro Ser Ser	
135	595 600 605	
136	tgt gtc ctg gag atc agc gtg cgg ggt gtg aag ata ggc gtc aag gcc	1872
137	Cys Val Leu Glu Ile Ser Val Arg Gly Val Lys Ile Gly Val Lys Ala	
138	610 615 620	
139	gat gac tcc cag gag gcc aag ggg aat aaa tgt agc cac ttt ttc cag	1920
140	Asp Asp Ser Gln Glu Ala Lys Gly Asn Lys Cys Ser His Phe Phe Gln	
141	625 630 635 640	
142	tta aaa aac atc tot ttc tgc gga tat cat cca aag aac aac aag tac	1968
143	Leu Lys Asn Ile Ser Phe Cys Gly Tyr His Pro Lys Asn Asn Lys Tyr	
144	645 650 655	
145	ttt ggg ttc atc acc aag cac ccc gcc gac cac cgg ttt gcc tgc cac	2016
146	Phe Gly Phe Ile Thr Lys His Pro Ala Asp His Arg Phe Ala Cys His	

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147          660          665          670
148 gtc ttt gtg tct gaa gac tcc acc aaa gcc ctg gca gag tcc gtg ggg      2064
149 Val Phe Val Ser Glu Asp Ser Thr Lys Ala Leu Ala Glu Ser Val Gly
150          675          680          685
151 aga gca ttc cag cag ttc tac aag cag ttt gtg gag tac acc tgc ccc      2112
152 Arg Ala Phe Gln Gln Phe Tyr Lys Gln Phe Val Glu Tyr Thr Cys Pro
153          690          695          700
154 aca gaa gat atc tac ctg gag tag ctgtgcagcc ccgccctctg cgtccccag      2166
155 Thr Glu Asp Ile Tyr Leu Glu
156          705          710
157 ccctcaggcc agtgccagga cagctggctg ctgacaggat gtggcactgc ttgaggaggg      2226
158 gcacctgcca ccgccagagg acaaggaagt gggggccgct ggcccagggt aggggaggg      2286
159 ggggcaatgg ggagaggcaa atgcagttaa ttgtaataata tgggattaga ttcattatg      2346
160 gagggcagag tgggctgcct ggggattggg agggacaggg cttggggagc aggtctctgg      2406
161 cagagaagga tgtccgttcc aggagcacac ggccctgccc catcctgggc cttacctccc      2466
162 ctgccagggc tcgggcgctg tggctcctgc cttgatgaag cccgtgtcct gccttgatga      2526
163 agcctgtgcc acctgcaagt gcccgccctg cccctgcccc acccccgaag accctgagct      2586
164 caggctgagc ccagccacct cccaaggact ttccagtagg aaatggcaac aggtgaagtc      2646
165 cctgttctca gctccgtcat ctggggtcgg gggctcctgc cactgacctc accggcatgc      2706
166 tggcctgtgg caggcctagg acctcaggcg gggaggagga gcgccagccc gtccgaaaag      2766
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168 caaaaaaaaaa      2836
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171 <211> LENGTH: 711
172 <212> TYPE: PRT
173 <213> ORGANISM: Homo sapiens
174 <400> SEQUENCE: 2
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176 1 5 10 15
177 Pro Ala Ala Ser Pro Phe Leu Gly Leu His Ile Ala Ser Pro Pro Asn
178 20 25 30
179 Phe Arg Leu Thr His Asp Ile Ser Leu Glu Glu Phe Glu Asp Glu Asp
180 35 40 45
181 Leu Ser Glu Ile Thr Asp Glu Cys Gly Ile Ser Leu Gln Cys Lys Asp
182 50 55 60
183 Thr Leu Ser Leu Arg Pro Pro Arg Ala Gly Leu Leu Ser Ala Gly Gly
184 65 70 75 80
185 Gly Gly Ala Gly Ser Arg Leu Gln Ala Glu Met Leu Gln Met Asp Leu
186 85 90 95
187 Ile Asp Ala Thr Gly Asp Thr Pro Gly Ala Glu Asp Asp Glu Glu Asp
188 100 105 110
189 Asp Asp Glu Glu Arg Ala Ala Arg Arg Pro Gly Ala Gly Pro Pro Lys
190 115 120 125
191 Ala Glu Ser Gly Gln Glu Pro Ala Ser Arg Gly Gln Gly Gln Ser Gln
192 130 135 140
193 Gly Gln Ser Gln Gly Pro Gly Ser Gly Asp Thr Tyr Arg Pro Lys Arg
194 145 150 155 160
195 Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln Asp Thr
196 165 170 175

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197  Leu Asn Asn Asn Ser Leu Gly Lys Lys His Ser Trp Gln Asp Arg Val
198              180              185              190
199  Ser Arg Ser Ser Ser Pro Leu Lys Thr Gly Glu Gln Thr Pro Pro His
200              195              200              205
201  Glu His Ile Cys Leu Ser Glu Glu Leu Pro Pro Gln Ser Gly Pro Ala
202              210              215              220
203  Pro Thr Thr Asp Arg Gly Thr Ser Thr Asp Ser Pro Cys Arg Arg Ser
204              225              230              235              240
205  Thr Ala Thr Gln Met Ala Pro Pro Gly Gly Pro Pro Ala Ala Pro Pro
206              245              250              255
207  Gly Gly Arg Gly His Ser His Arg Asp Arg Ile His Tyr Gln Ala Asp
208              260              265              270
209  Val Arg Leu Glu Ala Thr Glu Glu Ile Tyr Leu Thr Pro Val Gln Arg
210              275              280              285
211  Pro Pro Asp Ala Ala Glu Pro Thr Ser Ala Phe Leu Pro Pro Thr Glu
212              290              295              300
213  Ser Arg Met Ser Val Ser Ser Asp Pro Asp Pro Ala Ala Tyr Pro Ser
214              305              310              315              320
215  Thr Ala Gly Arg Pro His Pro Ser Ile Ser Glu Glu Glu Glu Gly Phe
216              325              330              335
217  Asp Cys Leu Ser Ser Pro Glu Arg Ala Glu Pro Pro Gly Gly Gly Trp
218              340              345              350
219  Arg Gly Ser Leu Gly Glu Pro Pro Pro Pro Arg Ala Ser Leu Ser
220              355              360              365
221  Ser Asp Thr Ser Ala Leu Ser Tyr Asp Ser Val Lys Tyr Thr Leu Val
222              370              375              380
223  Val Asp Glu His Ala Gln Leu Glu Leu Val Ser Leu Arg Pro Cys Phe
224              385              390              395              400
225  Gly Asp Tyr Ser Asp Glu Ser Asp Ser Ala Thr Val Tyr Asp Asn Cys
226              405              410              415
227  Ala Ser Val Ser Ser Pro Tyr Glu Ser Ala Ile Gly Glu Glu Tyr Glu
228              420              425              430
229  Glu Ala Pro Arg Pro Gln Pro Pro Ala Cys Leu Ser Glu Asp Ser Thr
230              435              440              445
231  Pro Asp Glu Pro Asp Val His Phe Ser Lys Lys Phe Leu Asn Val Phe
232              450              455              460
233  Met Ser Gly Arg Ser Arg Ser Ser Ser Ala Glu Ser Phe Gly Leu Phe
234              465              470              475              480
235  Ser Cys Ile Ile Asn Gly Glu Glu Gln Glu Gln Thr His Arg Ala Ile
236              485              490              495
237  Phe Arg Phe Val Pro Arg His Glu Asp Glu Leu Glu Leu Glu Val Asp
238              500              505              510
239  Asp Pro Leu Leu Val Glu Leu Gln Ala Glu Asp Tyr Trp Tyr Glu Ala
240              515              520              525
241  Tyr Asn Met Arg Thr Gly Ala Arg Gly Val Phe Pro Ala Tyr Tyr Ala
242              530              535              540
243  Ile Glu Val Thr Lys Glu Pro Glu His Met Ala Ala Leu Ala Lys Asn
244              545              550              555              560
245  Ser Asp Trp Val Asp Gln Phe Arg Val Lys Phe Leu Gly Ser Val Gln

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VERIFICATION SUMMARY

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